

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 14:18:50 / Search time 12.321 Seconds  
(without alignment)  
888.505 Million cell updates/sec

Title: US-10-757-832-2  
Perfect score: 8514  
Sequence: 1 MTPPEQAGQAGALALHAGK.....MVVTPPICFALGALMNNGC 1625

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 51470 seqs, 6736768 residues  
Total number of hits satisfying chosen parameters: 51470

Minimum DB-seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications\_AA\_New:  
1: /cgm2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /cgm2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgm2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgm2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /cgm2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /cgm2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgm2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgm2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	1.2	3690	US-10-995-561-1016	Sequence 1016, Ap
2	103.5	1.2	3714	US-10-995-561-1015	Sequence 1015, Ap
3	103.5	1.2	3717	US-10-821-234-1076	Sequence 1076, Ap
4	101	1.2	1306	US-10-467-657-5406	Sequence 5406, Ap
5	99.5	1.2	2828	US-11-080-991-54	Sequence 54, Appl
6	99.5	1.2	2828	US-11-186-284-49	Sequence 49, Appl
7	99	1.2	1307	US-10-995-561-711	Sequence 711, Ap
8	98	1.2	865	US-10-467-9628-33	Sequence 33, Appl
9	97.5	1.1	7102	US-11-143-980-48	Sequence 48, Appl
10	96	1.1	3655	US-11-075-185-5	Sequence 5, Appl1
11	95.5	1.1	3011	US-10-985-205-3	Sequence 3, Appl1
12	95	1.1	1206	US-10-995-561-709	Sequence 709, Appl
13	95	1.1	2256	US-11-144-368-4	Sequence 4, Appl1
14	95	1.1	5712	US-11-143-980-47	Sequence 47, Appl
15	93.5	1.1	820	US-10-467-657-4910	Sequence 4910, Ap
16	93	1.1	1806	US-10-995-561-912	Sequence 912, App
17	93	1.1	1806	US-10-995-561-915	Sequence 915, App
18	93	1.1	3674	US-11-000-463-454	Sequence 454, App
19	92.5	1.1	557	US-10-821-234-895	Sequence 895, App
20	92.5	1.1	882	US-11-012-762-34	Sequence 34, Appl
21	92	1.1	859	US-10-467-657-084	Sequence 6084, Ap
22	91.5	1.1	2004	US-10-467-657-84	Sequence 84, Appl
23	91.5	1.1	2004	US-10-467-657-6322	Sequence 6322, Ap
24	91.5	1.1	2059	US-11-087-100-4	Sequence 4, Appl1
25	91.5	1.1	2059	US-11-087-084-4	Sequence 4, Appl1

26	91.5	1.1	2059	US-11-087-085-4	Sequence 4, Appl1
27	91	1.1	423	US-10-793-626-3160	Sequence 3160, Ap
28	91	1.1	440	US-10-525-710-52	Sequence 52, Appl
29	90.5	1.1	468	US-10-467-657-3478	Sequence 3478, Ap
30	90.5	1.1	1304	US-10-821-234-1648	Sequence 1648, Ap
31	90.5	1.1	1572	US-11-143-980-46	Sequence 46, Appl
32	90	1.1	254	US-11-067-323-784	Sequence 784, App
33	90	1.1	3689	US-11-075-185-4	Sequence 4, Appl1
34	89.5	1.1	980	US-11-064-246-10	Sequence 10, Appl
35	89.5	1.1	1560	US-11-059-982-1	Sequence 1, Appl1
36	89.5	1.1	2101	US-10-857-780-23	Sequence 23, Appl
37	89	1.0	254	US-11-067-323-1107	Sequence 1107, Ap
38	89	1.0	530	US-11-055-822-256	Sequence 256, App
39	89	1.0	1432	US-10-510-386-218	Sequence 218, Appl
40	88.5	1.0	617	US-10-878-556A-67	Sequence 67, Appl
41	88.5	1.0	1389	US-10-467-657-334	Sequence 334, App
42	88	1.0	254	US-11-067-323-852	Sequence 852, App
43	87.5	1.0	305	US-11-080-091-2	Sequence 2, Appl1
44	87.5	1.0	519	US-11-080-991-106	Sequence 106, App
45	87	1.0	3063	US-11-186-284-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1					
US-10-995-561-1016					
Sequence 1016, Application US/10995561					
Publication No. US20050272054A1					
GENERAL INFORMATION:					
APPLICANT: CARGILL, Michele et al.					
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH					
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF					
TITLE OF INVENTION: DETECTION AND USES THEREOF					
FILE REFERENCE: C1001559					
CURRENT APPLICATION NUMBER: US/10/995,561					
CURRENT FILING DATE: 2004-11-24					
NUMBER OF SEQ ID NOS: 85702					
SOFTWARE: FASTSEQ for Windows Version 4.0					
SEQ ID NO 1016					
LENGTH: 3690					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-10-995-561-1016					
Query Match					
Best Local Similarity 18.4%; Pred. No. 11;					
Matches 248; Conservative 155; Mismatches 448; Indels 494; Gaps 65;					
QY	222	IIYALNAVIGRPIKMLASVKEPNIILIVYSCMTBSGIYVA-----LILALFLDI 273			
DB	2264	LILGTEATYGLH-AKTLIAAIRAVDRILSRILMSQGHGLANASPSGEOLRTIAVERLT 2322			
QY	274	FMTPEPVYKWMISIFGEWQAEQEPDXALDVVPTLLGGIGMAFGKXSTIGKXSTNSAL 333			
DB	2323	LME-----WRADLZGAPAAABKL 2342			
QY	334	KAAQENGKPAIRVFKQIMAWIPSEDPVPAALSNMEQAIKNECOLNQTAMLR--DRN 391			
DB	2343	AAAGRL-----LAVQEGSLWMBNQ-----ALAVQTRORLQAHGMDLAEALNRVADAT 2395			
QY	392	AGAEPLRLSDREBOE---VKKIAKCNASTTGTVA---LARISSARAAFEKARAEQT 445			
DB	2396	REAOBLNSRQBLERALKORKEISDNATLQATLHAARDTLASVFPLLSLDQAKER-- 2453			
QY	446	SRVRPVYKWSGRPGIGKTCFCQNLAKRIASIGDERSVGIIIPRAVDVHDYAGARVVL 505			
DB	2454	-----LRLASL-----DGARTPL 2468			
QY	506	WDFPGNDVVKALRLQMLADTCPTVTLNCDRIENKGRK--DSQVITITNQO--TPYPLD 562			
DB	2469	LQWQTFSPAGSLRLRVEAAEA-----HAQQLQALNLSITLIDVQDRLTQGAIE 2520			

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 14:13:00 / Search time 197.136 Seconds  
(without alignments)  
3444.190 Million cell updates/sec

Title: US-10-757-832-2

Perfect score: 8514  
Sequence: 1 MPPPOBAQPGALALHMEG.....MVPPTPICFALGALMNNGC 1625

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications, AA Main:  
1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8474	99.5	1625	US-10-757-832-2	Sequence 2, Appl1
2	3572	42.0	2179	US-10-314-739-2	Sequence 2, Appl1
3	343.5	4.0	1738	US-10-224-999A-3481	Sequence 3481, Ap
4	319	3.7	2227	US-09-929-955-12	Sequence 12, Appl
5	319	3.7	2227	US-10-104-966-12	Sequence 12, Appl
6	319	3.7	2227	US-10-719-619-12	Sequence 12, Appl
7	319	3.7	2227	US-10-817-591-12	Sequence 12, Appl
8	309	3.6	2227	US-10-135-988-2	Sequence 2, Appl1
9	304	3.6	2227	US-10-135-988-4	Sequence 4, Appl1
10	302	3.5	2227	US-10-135-988-6	Sequence 6, Appl1
11	190.5	2.2	458	US-10-770-600-53	Sequence 53, Appl
12	177.5	2.1	1285	US-10-424-559-265913	Sequence 265913,
13	177	2.1	652	US-10-472-459-48	Sequence 48, Appl
14	173.5	2.0	516	US-11-051-613-48	Sequence 48, Appl
15	173.5	2.0	516	US-10-352-393-13	Sequence 13, Appl
16	152.5	1.8	627	US-10-222-100-3	Sequence 3, Appl1
17	150	1.8	1133	US-10-156-761-11645	Sequence 11645, A
18	148.5	1.7	512	US-10-352-393-12	Sequence 12, Appl
19	148.5	1.7	7349	US-10-314-657-46	Sequence 46, Appl
20	148.5	1.7	7349	US-10-473-193-46	Sequence 46, Appl
21	142.5	1.7	3816	US-09-808-880-3	Sequence 3, Appl1
22	142.5	1.7	3816	US-10-732-923-20544	Sequence 20544, A
23	140	1.6	2420	US-10-437-963-163599	Sequence 163599,
24	131	1.5	1601	US-10-437-963-195646	Sequence 195646,
25	126.5	1.5	274	US-10-425-115-354307	Sequence 354307,
26	125	1.5	527	US-10-684-129-8	Sequence 8, Appl1
27	124.5	1.5	460	US-10-282-122A-61203	Sequence 61203, A

28	124.5	1.5	1974	4	US-10-369-493-5455	Sequence 5455, Ap
29	124	1.5	3753	3	US-09-980-217-29	Sequence 29, Appl
30	123	1.4	19608	4	US-10-084-846A-8	Sequence 8, Appl1
31	122.5	1.4	2063	3	US-09-918-715-204	Sequence 204, App
32	122.5	1.4	2063	4	US-10-474-794-204	Sequence 204, App
33	122.5	1.4	2063	5	US-10-979-159-204	Sequence 204, App
34	122	1.4	2379	5	US-10-211-028-7	Sequence 7, Appl1
35	122	1.4	2639	5	US-10-450-763-45375	Sequence 45375, A
36	121	1.4	764	4	US-10-369-493-18081	Sequence 18081, A
37	121	1.4	764	4	US-10-389-566-1010	Sequence 1010, Ap
38	119.5	1.4	4572	5	US-10-042-665A-4	Sequence 4, Appl1
39	119.5	1.4	4599	3	US-09-976-059-15	Sequence 15, Appl
40	119	1.4	826	5	US-10-732-923-6777	Sequence 6777, Ap
41	119	1.4	1387	4	US-10-156-761-13000	Sequence 13000, A
42	118.5	1.4	799	4	US-10-369-493-10623	Sequence 10623, A
43	118	1.4	926	4	US-10-282-122A-62076	Sequence 62076, A
44	118	1.4	1217	4	US-10-369-493-11861	Sequence 11861, A
45	118	1.4	2220	4	US-10-389-566-802	Sequence 802, App

## ALIGNMENTS

RESULT 1  
US-10-757-832-2  
Sequence 2, Application US/10757832  
Publication No. US20050037016A1  
GENERAL INFORMATION:  
APPLICANT: VIRGIN, HERBERT W.  
TITLE OF INVENTION: MORINE CALICIVIRUS  
FILE REFERENCE: 56029-45752  
CURRENT APPLICATION NUMBER: US/10/757,832  
CURRENT FILING DATE: 2004-01-14  
PRIOR APPLICATION NUMBER: 60/440,016  
PRIOR FILING DATE: 2003-01-14  
NUMBER OF SEQ ID NOS: 54  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 1625  
TYPE: PRT  
ORGANISM: Murine Norovirus type 1  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (145)..(145)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (282)..(282)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (299)..(299)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (316)..(316)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (327)..(327)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (453)..(453)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (544)..(544)  
OTHER INFORMATION: Variable amino acid  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (559)..(559)  
OTHER INFORMATION: Variable amino acid



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:39:53 : Search time 273.799 seconds

4187.310 Million cell updates/sec

Title: US-10-757-832-2

```

reflect score: 8514
Sequence: 1 MTPPEOEAOFGAIAIHAEG MMRTPRRCENTCAIYVCC 100

```

Scoring table: BIOSUM62

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

```
Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_tramb1.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	84.47	99.2	1640	2	080J95_9CALI	080J95 murine norovirus
2	3790.5	44.5	1639	2	06PPX1_9CALI	06PPX1 norovirus h
3	3786.5	44.5	1639	2	06PPW5_9CALI	06PPW5 norovirus h
4	3786.5	44.5	1639	2	06PPW8_9CALI	06PPW8 norovirus h
5	3786.5	44.5	1639	2	06PP65_9CALI	06PP65 human calicivirus
6	3785.5	44.5	1639	2	06PPW2_9CALI	06PPW2 norovirus h
7	3785.5	44.5	1639	2	06PPX4_9CALI	06PPX4 norovirus h
8	3785.5	44.5	1639	2	06PPY7_9CALI	06PPY7 norovirus h
9	3785.5	44.5	1639	2	06PPY0_9CALI	06PPY0 norovirus h
10	3784.5	44.5	1639	2	08BU10_9CALI	08BU10 norwalk-11k
11	3784.5	44.5	1639	2	06JRGV_9CALI	06JRGV norovirus g
12	3783.5	44.4	1597	2	08JUV3_9CALI	08JUV3 norovirus g
13	3781.5	44.4	1639	2	06RWM2_9CALI	06RWM2 norwalk-11k
14	3774.5	44.3	1639	2	08OR07_9CALI	08OR07 norovirus g
15	3770.5	44.3	1639	2	08X18_9CALI	08X18 snow mounta
16	3769	44.3	1639	2	08X16_9CALI	08X16 norwalk-11k
17	3768.5	44.3	1639	2	09W183_9CALI	09W183 camberwell
18	3766.5	44.2	1639	1	POLN1ORDY	P546103 a non-atric
19	3765.5	44.2	1639	1	068103_9CALI	068103 hawaii calicivirus
20	3764.5	44.2	1639	2	076MP6_9CALI	076MP6 norwalk-11k
21	3763.5	44.2	1639	2	091PN3_9CALI	091PN3 norwalk-11k
22	3761.5	44.2	1639	2	08RBM2_9CALI	08RBM2 norwalk vir
23	3761.5	44.2	1639	2	08VOP3_9CALI	08VOP3 human calicivirus
24	3760.5	44.2	1639	2	06XD14_9CALI	06XD14 human calicivirus
25	3757.5	44.1	1697	2	05URYP7_9CALI	05URYP7 human calicivirus
26	3754.5	44.1	1702	2	05U928_9CALI	05U928 norovirus h
27	3752.5	44.1	1702	2	08UX14_9CALI	08UX14 norwalk-11k
28	3750.5	44.1	1702	2	08XJ15_9CALI	08XJ15 norwalk-11k
29	3735.5	43.9	1639	2	05XP12_9CALI	05XP12 norovirus h
30	3572	42.0	1788	2	083883_9CALI	083883 norwalk vir
31	3560	41.8	1788	1	POLN1SOUV	004544 s non-atric

## ALIGNMENTS

32	3556	41.8	1788	2	08JVV6_9CAL1	08JVV6	norwalk-11k
33	3543	41.6	1785	2	08DU47_9CAL1	08DU47	chalka virus
34	3538	41.6	1787	2	08UXJ1_9CAL1	08UXJ1	norwalk-11k
35	3529.5	41.5	1784	2	09YS15_9CAL1	09YS15	norwalk vir
36	3472	40.8	1680	2	09IQ23_9CAL1	09IQ23	bovine calic
37	2225	26.1	838	2	07OE73_9CAL1	07OE73	norwalk vir
38	1608.5	18.9	540	2	05DIP2_9CAL1	05DIP2	norwalk vir
39	1571.5	18.5	534	2	05MA18_9CAL1	05MA18	norovirus h
40	1435.5	16.9	480	2	06BS36_9CAL1	06BS36	norovirus h
41	1384.5	16.3	462	2	07TB12_9CAL1	07TB12	bovine ente
42	1377.5	16.2	462	2	07TBK8_9CAL1	07TBK8	bovine ente
43	1129	13.3	333	2	089164_9CAL1	089164	norovirus i
44	973	11.4	333	2	066292_9CAL1	066292	human calic
45	830	9.7	289	2	0911H0_9CAL1	0911H0	human calic

## RESULT 1

ID 080395 9CALI PRELIMINARY; PRT, 1640 AA.  
 AC 080395/  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Polypotein.  
 DE Murine norovirus 1.  
 OS  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;  
 NCBI\_NCBIdb:223397;  
 OX NCBI [1]  
 RN  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22511930; PubMed=12624267; DOI=10.1126/science.1077905;  
 RX Kertel S.M., Wobus C.E., Lay M., Davidson J., Virgin H.W.;  
 RT "STAT1-dependent innate immunity to a Norwalk-like virus.";  
 RL EMBL; AY228235; AAO63098.1; -; Genomic\_RNA.  
 DR HSSP; P27410; 1KHV.  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004197; P:cysteine-type endopeptidase activity; IEA.  
 DR GO; GO:0003723; P:RNA binding; IEA.  
 DR GO; GO:0003724; P:RNA helicase activity; IEA.  
 DR GO; GO:0003968; P:RNA-directed RNA polymerase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR GO; GO:0006350; P:transcription; IEA.  
 DR GO; GO:0019079; P:viral genome replication; IEA.  
 DR InterPro; IPR000585; Hemopepin.  
 DR InterPro; IPR001665; Peptidase C37.  
 DR InterPro; IPR004004; Pept Calci.  
 DR InterPro; IPR000605; RNA helicase.  
 DR InterPro; IPR007095; RNA\_pol\_DS\_PS.  
 DR InterPro; IPR001205; RNA\_pol\_F3D.  
 DR InterPro; IPR007094; RNA\_pol\_PSVlr.  
 DR Pfam; PF05416; Peptidase C37; 1.  
 DR Pfam; PF00680; RdRP 1; 1.  
 DR Pfam; PF00910; RNA helicase; 1.  
 DR PRINTS; PR00918; Caliciviruses.  
 DR PRINTS; PR00917; SRVCTSPFAS.  
 DR PROSITE; PS00024; HEMOPEPIN; 1.  
 KW Polypeptin.  
 QO SEQUENCE 1640 AA; 182311 MW; 2D9E9C9C88BBAF6D CTR664.

Query Match	Score	DB 2	Length
99.2%	8447	1640	

QY 1 MTPBQSAQPGALAAHAEGPLAGLPVTRSDAVLIENEBERRKSDPWLRIDMSDAIF 60

Db 1 MTPBQSAQPGALAAHAEGPLAGLPVTRSDAVLIENEBERRKSDPWLRIDMSDAIF 60

QY 61 RRYHPLPKSDRPAPSHADANDAKSPVIGSLIEDDHKFTYHYSVYIGGLVGVNNS 120

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:42:44 / Search time 49.2839 Seconds  
(without alignments)  
3172.480 Million cell updates/sec

Title: US-10-757-832-2

Perfect score: 8514  
Sequence: 1 MTPPEQBAQPGALALHAEG.....MVPPTPICPALGALMNNGC 1625

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: PIR 80: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3560	41.8	1737	2 A37491	hypothetical helic
2	995	11.7	306	2 E37471	hypothetical helic
3	973	11.4	333	2 S60615	RNA-directed RNA p
4	850.5	10.0	352	2 C37471	hypothetical helic
5	769.5	9.0	1763	1 RRMW9	genome polypotein
6	760.5	8.9	1762	2 T09245	genome polypotein
7	731.5	8.6	2344	2 S55389	genome polypotein
8	717.5	8.4	2344	2 S55389	genome polypotein
9	711	8.4	1287	2 A43488	genome polypotein
10	709.5	8.3	2344	1 RRMW9	genome polypotein
11	523.5	6.1	211	2 D37471	hypothetical helic
12	381	4.5	2292	1 S55401	hypothetical helic
13	375	4.4	2292	1 GNNYB	genome polypotein
14	372	4.4	2292	1 GNNYB	genome polypotein
15	371.5	4.4	2303	1 GNNYB	genome polypotein
16	370.5	4.4	2292	2 S35961	capsid polypotein
17	361.5	4.2	2301	1 GNNYB	genome polypotein
18	361	4.2	2303	1 GNNYB	genome polypotein
19	361	4.2	2303	1 S13554	genome polypotein
20	359.5	4.2	2290	1 GNNYB	genome polypotein
21	347.5	4.1	2175	1 GNNYB	genome polypotein
22	326	3.8	2214	1 A48548	genome polypotein
23	324	3.8	2205	1 GNNYB	genome polypotein
24	324	3.8	2205	1 GNNYB	genome polypotein
25	320	3.8	2164	1 GNNYB	genome polypotein
26	319	3.7	2207	1 S09553	genome polypotein
27	319	3.7	2227	1 GNNYB	genome polypotein
28	318.5	3.7	381	2 A40481	RNA-directed RNA p
29	313	3.7	2194	1 GNNYB	genome polypotein

30	312	3.7	2333	1 GNNYB	genome polypotein
31	310	3.6	2206	1 GNNYB	genome polypotein
32	310	3.6	2207	1 GNNYB	genome polypotein
33	309.5	3.6	2230	1 GNNYB	genome polypotein
34	309	3.6	2237	1 GNNYB	genome polypotein
35	308.5	3.6	2332	1 GNNYB	genome polypotein
36	307	3.6	2150	1 GNNYB	genome polypotein
37	306.5	3.6	2332	1 GNNYB	genome polypotein
38	305.5	3.6	2206	2 S03822	genome polypotein
39	305	3.6	2157	1 GNNYB	genome polypotein
40	305	3.6	2209	1 GNNYB	genome polypotein
41	305	3.6	2336	2 S37077	genome polypotein
42	304	3.6	2227	1 GNNYB	genome polypotein
43	303.5	3.6	2207	1 GNNYB	genome polypotein
44	303.5	3.6	2227	1 GNNYB	genome polypotein
45	302	3.5	2179	1 GNNYB	genome polypotein

#### ALIGNMENTS

#### RESULT 1

A37491 hypothetical helicase/polymerase polypotein - Southampton virus

N/Alternate names: orf1 protein

C/Species: Southampton virus

C/Date: 03-Mar-1994 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C/Accession: A37491

R/Lambden, P.R.; Caul, E.O.; Ashley, C.R.; Clarke, I.N.

Science 259, 516-519, 1993

A/Title: Sequence and genome organization of a human small round-structured (Norwalk-like

A/Reference number: A37491, PMID:93142023; PMID:8380940

A/Content: small round-structured virus, SRSV, Norwalk virus, Norwalk-like virus, SRSV

A/Accession: A37491

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: genomic RNA

A/Residue: 1-1737 <LAMB>

A/Cross-reference: UNIPROT:004544; UNIPARC:UP100001757D7

A/Note: sequence extracted from NCBI backbone (NCBI:123456)

C/Superfamily: rabbit calicivirus RNA polypotein

Query Match	41.8%	Score 3560; DB 2; Length 1737;
Best Local Similarity	44.0%	Pred. No. 8.6e-245;
Matches 713; Conservative 270; Mismatches 512; Indels 126; Gaps 20;		
QY	73	PDAPSHADAMDAKPEVIGSLBDDKFTYHYVYIGGLVMGVNNSAIVCOATTIVEK 132
DB	126	FLPPIDLRNRPASBPFTIGMIEFYRGHIVHSIYIGQGTGVHSPQAPASVAVTIOP 185
QY	133	LHLMPVW--BPRXPLDSALKKCVGMTVPVATVNCVOCWIVIGIDTWLKRKIS 190
DB	186	IAAMWVCITPQKHKRISTDQKLENEBPVVAITNCFPCQVNNLSDITMLQRLVT 245
QY	191	RDLPFYSVVDWNVDDQEPFIPSKLNVSDGILVALSAVGRPIKMLASVKEPNIINIV 250
DB	246	SG-RFHHPQWSQCPPEPQDSKELIVRDALLAANGVLSQPKNVLGLKPLNVNITL 304
QY	251	LSQDWTFSQIVNALILALFDFITPPTVTKMISIFGWOABGPDXALDVPTLLGG 310
DB	305	SNDQMTFMGVENVILLBLFGVFNPPDVNSITASLDPFNLQGPDLRLDLPVILGG 364
QY	311	IGNAPGLXSETIKRKLXSTUSALKAQWKGKPIVVKQIMAMTWPEEDVPALLSMNQ 370
DB	365	IGLALGFTNDKVKVWMSAVDGLAANTQDQYGLSIFSLIKTFF-CGDDQERTLKIGEA 423
QY	371	AIINKSCOLENQLTAMLRDNAGAPLRSIDBEOBVRKLIACGNSATYGTNALARI 430
DB	424	AVIDMVLSTSTQVLVRDQAKAMNLLDNBERRKLSANRADPHVISTTALSLRI 483
QY	431	SNAPAAFEKAPAGQSRVRFVVMVSGRPGIGTCPCQNLAKIILASLDGTSVGIIPRA 490
DB	484	SNARSLAKAQAEMTSRMFPVIVMCGPPIGKTKAAEHIAKLAIIEIRPGKVLVPR 543

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 14:12:48, Search time 60.2359 seconds

(without alignments)  
2230.364 Million cell updates/sec

Title: US-10-757-832-2

Sequence: 1 MTPPQBAQPGALAHMG.....MVPFPICFALGALNNGC 1625

Scoring table:

BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/7\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/8\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/9\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3572	42.0	1738	2	US-08-486-049-2
2	3572	42.0	1738	2	US-10-314-739A-2
3	379.5	4.5	126	2	US-10-314-739A-7
4	319	3.7	2227	2	US-10-104-966-12
5	319	3.7	2227	2	US-09-929-955-12
6	315	3.7	2232	2	US-09-091-219-25
7	315	3.7	2232	2	US-09-660-541-25
8	315	3.7	2247	2	US-09-091-219-2
9	315	3.7	2247	2	US-09-660-541-2
10	310	3.6	2206	1	US-07-852-260-2
11	310	3.6	2206	1	US-08-461-503-2
12	310	3.6	2206	1	US-08-465-250-2
13	309	3.6	2227	2	US-08-475-886-2
14	309	3.6	2227	2	US-08-397-232-2
15	309	3.6	2227	2	US-09-171-387-2
16	309	3.6	2227	2	US-09-653-499-2
17	309	3.6	2227	2	US-10-135-988-2
18	306	3.6	2318	2	US-09-091-219-24
19	306	3.6	2318	2	US-09-660-541-24
20	304	3.6	2227	2	US-08-475-886-4
21	304	3.6	2227	2	US-09-653-499-4
22	304	3.6	2227	2	US-10-135-988-4
23	302	3.5	2227	2	US-08-475-886-6
24	302	3.5	2227	2	US-08-397-232-4
25	302	3.5	2227	2	US-09-653-499-6
26	302	3.5	2227	2	US-10-135-988-6
27	204	2.4	3457	1	US-08-416-603-4

28	194.5	2.3	3443	1	US-08-416-603-2	Sequence 2, Appl
29	177	2.1	652	2	US-10-272-459-48	Sequence 48, Appl
30	174	2.0	1416	1	US-08-061-465-4	Sequence 4, Appl
31	173.5	2.0	516	2	US-09-496-320-13	Sequence 1, Appl
32	163	1.9	495	6	5516630-4	Patent No. 5516630
33	152.5	1.8	627	2	US-10-222-100-3	Sequence 3, Appl
34	148.5	1.7	512	2	US-09-496-320-12	Sequence 12, Appl
35	142.5	1.7	3816	2	US-09-428-517-3	Sequence 3, Appl
36	126	1.5	1090	2	US-09-902-540-15442	Sequence 15442, A
37	125.5	1.5	126	2	US-10-314-739A-14	Sequence 14, Appl
38	125	1.5	527	2	US-09-900-920-61	Sequence 61, Appl
39	119.5	1.4	4572	2	US-10-042-665A-4	Sequence 4, Appl
40	118	1.4	314	2	US-09-583-545-15	Sequence 15, Appl
41	117	1.4	314	2	US-09-514-245-24	Sequence 24, Appl
42	117	1.4	566	2	US-09-514-245-18	Sequence 18, Appl
43	117	1.4	703	2	US-09-902-540-11194	Sequence 11194, A
44	117	1.4	4630	2	US-09-091-609-2	Sequence 2, Appl
45	117	1.4	5215	2	US-09-105-537-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-486-049-2  
Sequence 2, Application US/08486049  
Patent No. 6572862  
GENERAL INFORMATION:  
APPLICANT: Bates, Mary K  
APPLICANT: Jiang, Xi  
TITLE OF INVENTION: Methods and Reagents to Detect and  
NUMBER OF INVENTION: Characterize No. 6572862walk and Related Viruses  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fulbright & Jaworski L.L.P.  
STREET: 801 Pennsylvania Ave., N.W.  
CITY: Washington, D.C.  
STATE:  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,049  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Davis, Peter  
REGISTRATION NUMBER: 36,119  
REFERENCE/DOCKET NUMBER: 311,023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-662-0200  
TELEFAX: 202-662-4643  
TELEX:  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1738 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-049-2  
Query Match 42.0%; Score 3572; DB 2; Length 1738;  
Best Local Similarity 44.2%; Pred. No. 0;  
Matches 720; Conservative 257; Mismatches 517; Indels 136; Gaps 20;  
66 LRPKRDPAASHDANDAKRPVIGILBDHKKFYHYSVYIGGLWGVNPNPAAVQC 125  
126 LRPVDRSTP-----ATEPTIGDIWEFTYEGHIVYALYIGGKIVGVHSPDAPRSI 177

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:42:44 ; Search time 16.4078 Seconds  
(without alignments) 3172.480 Million cell updates/sec

Title: US-10-757-832-3

Sequence: 1 MRMDGAPKANGSEBASGD.....PRVQLASVLSLANGRMKQ 541

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir60:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	992.5	35.0	542	2 S60616	capsid protein - h
2	980	34.5	539	2 S40111	capsid protein - h
3	970.5	34.2	546	2 B37491	major capsid prote
4	958.5	33.8	530	2 B37471	capsid protein - N
5	310.5	10.9	576	2 A53982	capsid protein - E
6	308.5	10.9	702	1 A48562	coat protein - San
7	306.5	10.8	2344	2 S55399	genome polypotein
8	301.5	10.6	2344	2 S64740	genome polypotein
9	300.5	10.6	2344	1 RRMWRH	genome polypotein
10	278	9.8	703	1 C48562	coat protein - San
11	264.5	9.3	668	1 VCMWPC	coat protein - fel
12	250	8.8	668	2 JQ2354	capsid protein - f
13	249	8.7	671	1 VCMWF9	coat protein - fel
14	246	8.8	668	2 JQ2356	capsid protein - f
15	241	8.5	668	1 VCMWF9	coat protein - fel
16	135	4.8	757	2 JS0198	genome polypotein
17	120	4.2	733	2 JQ1892	capsid protein - f
18	120	4.2	2336	2 S37077	genome polypotein
19	117.5	4.1	2332	1 GNNYF	genome polypotein
20	116.5	4.1	733	2 JQ1891	capsid protein - f
21	116.5	4.1	2333	1 GNNY2P	genome polypotein
22	115.5	4.1	511	2 C70803	hypothetical prote
23	112	3.9	3473	1 A46112	genome polypotein
24	112	3.9	3473	2 S27927	polyprotein - rice
25	111	3.9	1324	2 S06187	RNA2 polypotein -
26	110.5	3.9	1011	1 GNNY1	genome polypotein
27	109.5	3.9	1693	1 MAMWHE	genome polypotein
28	109	3.8	329	2 C97560	hypothetical prote
29	109	3.8	329	2 AB2781	amidohydrolase (im

30	108.5	3.8	2292	2 S35961	capsid polypotein
31	108	3.8	2194	1 GNNY87	genome polypotein
32	105	3.7	2332	2 GNNY4P	genome polypotein
33	105	3.7	3573	2 S23070	erythronolide synt
34	104.5	3.7	1706	2 B75633	probable RNA helic
35	104	3.7	575	2 T11753	mullerian inhibiti
36	103.5	3.6	476	2 T42692	hypothetical prote
37	103.5	3.6	1686	2 A87692	conserved hypotet
38	103.5	3.6	2206	2 S03822	genome polypotein
39	103.5	3.6	2292	1 GNNY8B	genome polypotein
40	103.5	3.6	2292	2 S55401	capsid polypotein
41	103	3.6	1809	2 S57329	tuberosus sclerosi
42	101.5	3.6	2206	1 GNNY4P	genome polypotein
43	101.5	3.6	2206	1 GNNY27	genome polypotein
44	100.5	3.5	647	2 T35931	probable gamma-glu
45	100	3.5	307	2 B83129	homoprotocatechua

## ALIGNMENTS

## RESULT 1

S60616  
capsid protein - human calicivirus (strain Melksham)  
C:Species: human calicivirus  
A:Variety: strain Melksham  
C:Date: 23-May-1997 #sequence\_revision 23-May-1997 #text\_change 09-Jul-2004  
C:Accession: S60616  
R:Green, S.M.; Lambden, P.R.; Gaul, E.O.; Ashley, C.R.; Clarke, I.N.  
Virus Res. 37, 271-283, 1995  
A>Title: Capsid diversity in small round-structured viruses: molecular characterization  
A:Reference number: S60615; MUID:9613658; PMID:8533462  
A:Accession: S60616  
A:Molecule type: genomic RNA  
A:Residues: 1-542 <GR>  
A:Cross-references: UNIPROT:066293; UNIPARC:U0100000ED1P; EMBL:X01879; NID:9976077; PI  
A:Experimental source: strain Melksham  
A>Note: It is uncertain whether Met-1 or Met-3 is the initiator  
C:Superfamily: human calicivirus capsid protein  
C:Keywords: capsid protein; coat protein

Query Match 35.0%; Score 992.5; DB 2; Length 542;  
Best Local Similarity 42.0%; Pred. No. 2.3e-71;  
Matches 233; Conservative 79; Mismatches 208; Indels 35; Gaps 14;

QY	1	MEM-SDGAPKANGSEBASGODIVPAVNAEQVAKXQVPAAGALAPAAAGQINQIXPMTFQNP	59
DB	1	MEMASNDAPSTDG--AAG--LVPSNNVMALEPVAGALAPVGTQNTIIDPMTIRANP	56
QY	60	VCCPIGEPISPRNTPGELIPDLALGPNPYLAHLSAMVYGVGNKXEVQLVLGNAFTA	119
DB	57	VQAPNGEFTVSPRANRGEVILNLELPELNPILAHARNTYAGCMETQVWMLAGNAFTA	116
QY	120	GRVVVALVPPYPPKSLTAAQITCEPHWCDVRTTEPIQLPLDVRVLMHATQDBESM	179
DB	117	GLVPAVAPHPPEVNTLSPQKITMFPVILIDVRLTEPVLLPDPVANSFHHYQKDDPKM	176
QY	180	RIVCMULTYPLRNSSQEDBSFVSGRLSKPADPNNVYLTLPPIERTYMMVDPVQPLR	239
DB	177	RIVAMLYPLRNSGSDDVFTVSCRVTTRSPDPFDYVLPVPSKTEFTLPIILGSR	236
QY	240	CHHARWPAVYGLVDPSPNPNQNGRHHVHVGTLTGTTPLSGSVWSCPAKXAAYKFS	299
DB	237	LSNSRFPVVIDQMTYSFNVISVQCGNGCTIDGELQSTTQGVSGICAFKGVTAHMD	296
QY	300	GTGCVATFTLLIDQSGAAYVG--DRAAPGLPFRFLMATGDRGPDRIHQWRQAGH----	353
DB	297	NDHLANNVTITNNGSPFPDSBDIPALGVPPFOGKRVFVVISQDRKON--AAGHSBPAN	352
QY	354	--HFMILGPTTNADQAPQGRVFAVSVTAAALSDLVGKRVAVRISYIGQDT-----	404
DB	353	RGHDAVV--FTYTAQYTPKGOIQIGTQOTDDL--TVNQPVKCTP--VGLNTEHFNQWV	406



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:39:53 ; Search time 91.1542 Seconds

(without alignments)  
4187,310 Million cell updates/sec

Title: US-10-757-832-3

Perfect score: 2838

Sequence: 1 MRMSDGAAPRANGSEASGOD.....PRLYOLASVSLATGEMTXQ 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_05.80.\*

2: uniprot\_sprot.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2830	99.7	541	2	080J94_9CALI	080J94 murine norovirus
2	1036.5	36.5	556	2	0917V6_9CALI	0917V6 norwalk-11k
3	1036.5	36.5	556	2	09PY75_9CALI	09PY75 human calicivirus
4	1035.5	36.5	556	2	0917V9_9CALI	0917V9 norwalk-11k
5	1027	36.2	543	2	091V43_9CALI	091V43 human calicivirus
6	1024	36.1	554	2	08BC66_9CALI	08BC66 human calicivirus
7	1021.5	36.0	555	2	08BAC5_9CALI	08BAC5 human calicivirus
8	1015	35.8	540	2	06BAX6_9CALI	06BAX6 norovirus
9	1013	35.7	540	2	06BAX9_9CALI	06BAX9 norovirus
10	1012	35.7	543	2	0918B9_9CALI	0918B9 norwalk-11k
11	1003	35.3	540	2	08BC85_9CALI	08BC85 human calicivirus
12	1002.5	35.3	540	2	09Y814_9CALI	09Y814 norwalk-11k
13	1002.5	35.3	542	2	0913B6_9CALI	0913B6 human calicivirus
14	993.5	35.0	542	2	012305_9CALI	012305 snow mountain
15	993.5	35.0	542	2	080R06_9CALI	080R06 snow mountain
16	992.5	35.0	539	2	08JVV5_9CALI	08JVV5 norwalk-11k
17	992.5	35.0	542	2	066293_9CALI	066293 human calicivirus
18	991	34.9	535	2	0915C6_9CALI	0915C6 human calicivirus
19	990	34.9	535	2	090MK6_9CALI	090MK6 chitrea virus
20	989.5	34.9	542	2	05TKU0_9CALI	05TKU0 norovirus
21	987.5	34.8	541	2	091V42_9CALI	091V42 human calicivirus
22	985.5	34.7	542	2	096877_9CALI	096877 snow mountain
23	985	34.7	535	2	076MP5_9CALI	076MP5 norwalk-11k
24	985	34.7	535	2	091115_9CALI	091115 human calicivirus
25	985	34.7	535	2	054AD6_9CALI	054AD6 norwalk-11k
26	985	34.7	539	2	08VDP6_9CALI	08VDP6 human calicivirus
27	983	34.6	535	2	0917V3_9CALI	0917V3 norwalk-11k
28	982.5	34.6	544	2	0918C5_9CALI	0918C5 norwalk-11k
29	982	34.6	539	1	068537_9CALI	068537 norovirus
30	981	34.6	539	2	077Q81_9CALI	077Q81 camberwell
31	981	34.6	539	2	077Q81_9CALI	077Q81 camberwell

32	981	34.6	539	2	08VDP2_9CALI	08VDP2 human calic
33	980.5	34.5	539	2	08JW43_9CALI	08JW43 norwalk-11k
34	980.5	34.5	540	2	0915C8_9CALI	0915C8 human calic
35	980.5	34.5	544	2	09DU46_9CALI	09DU46 chiba virus
36	980.5	34.5	544	2	090TE7_9CALI	090TE7 chiba virus
37	980	34.5	539	2	06287_9CALI	06287 calicivirid
38	980	34.5	540	2	06DMP9_9CALI	06DMP9 norovirus b
39	979.5	34.5	539	2	05GHH7_9CALI	05GHH7 norovirus n
40	979.5	34.5	540	2	06REM4_9CALI	06REM4 norovirus g
41	979	34.5	535	2	0917X7_9CALI	0917X7 norwalk-11k
42	979	34.5	546	2	091V47_9CALI	091V47 human calic
43	978.5	34.5	539	2	091SD0_9CALI	091SD0 human calic
44	977.5	34.4	539	2	05GHH4_9CALI	05GHH4 norovirus b
45	977.5	34.4	540	2	06PPK0_9CALI	06PPK0 norovirus h

## ALIGNMENTS

RESULT 1	
ID	080J94_9CALI PRELIMINARY; PRT; 541 AA.
AC	080J94_9CALI
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DS	Capaid protein.
OC	Murine norovirus 1.
OC	Virusess; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC	Norovirus.
OX	NCHI_TextID=223997;
OX	NCHI_TextID=223997;
OX	NCHI_TextID=223997;
RP	NCHI_TEXTID SEQUENCE.
RX	MEDLINE=225119301. PubMed=12624267; DOI=10.1126/science.1077905;
RA	Karst S.M., Mobus C.B., Lay M., Davidson J., Virgin H.W.;
RT	"STAT1-dependent innate immunity to a Norwalk-like virus.";
RL	Science 289:1575-1578(2003).
DR	EMBL, AY228225; AAC63099.1 - Genomic_RNA.
DR	InterPro; IPR004005; Calci1_coat.
DR	Pfam; PF00915; Calci1_coat; 1.
DR	SEQUENCE 541 AA; 58895 MW; CEF8BF8345B9A541 CRC64;
Query Match	99.7%; Score 2830; DB 2; Length 541;
Best Local Similarity	100.0%; Pred. No. 1.2e-222;
Matches	541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MRMSDGAAPRANGSEASGODLVPAVEAOPXOPVAGALAPAGCINOIXPWIPONFV 60
DB	1 MRMSDGAAPRANGSEASGODLVPAVEAOPXOPVAGALAPAGCINOIXPWIPONFV 60
QY	61 OCPLGSPSISPRNTPEBILFDLALGPNLYLAHLSMTTGVGNKEVQVLGNATFTAG 120
DB	61 OCPLGSPSISPRNTPEBILFDLALGPNLYLAHLSMTTGVGNKEVQVLGNATFTAG 120
QY	121 KVVVALVPPPPGSLTTQOITCEPHVMCDVRLPELOQLDLVRRVLAATDOESMR 180
DB	121 KVVVALVPPPPGSLTTQOITCEPHVMCDVRLPELOQLDLVRRVLAATDOESMR 180
QY	181 LVCMALTYPLRTNSPGDESFFVSGRLSKPAADNFVYLPPIERTTYRMVDLPVIOBLC 240
DB	181 LVCMALTYPLRTNSPGDESFFVSGRLSKPAADNFVYLPPIERTTYRMVDLPVIOBLC 240
QY	241 THARWAPVYVGLVDPSPBPNPOMONGRVAVDGTILGTTBISGSWVSCFAXBAAYKQSG 300
DB	241 THARWAPVYVGLVDPSPBPNPOMONGRVAVDGTILGTTBISGSWVSCFAXBAAYKQSG 300
QY	301 TGSAVATFTLLBOGSAVYVGDRAAPVGLPEPLATGDRGRDHODRQAGHFFETIG 360
DB	301 TGSAVATFTLLBOGSAVYVGDRAAPVGLPEPLATGDRGRDHODRQAGHFFETIG 360
QY	361 PTTNADQAPYQGVAFVTAALASLDVDSGRVRAVPSIYGFODTIBEYNDGLVPLAPPI 420
DB	361 PTTNADQAPYQGVAFVTAALASLDVDSGRVRAVPSIYGFODTIBEYNDGLVPLAPPI 420



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 14:13:00 / Search time 65.631 Seconds  
(without alignments)  
3444.190 Million cell updates/sec

Title: US-10-757-832-3

Perfect score: 2838  
Sequence: 1 MRMSDGAAPRANGSEASGCD.....PRUYQLASVGLATGRMLKQ 541

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

Published Applications AA Main:  
1: /cgm2\_6/ptcdat1/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgm2\_6/ptcdat1/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgm2\_6/ptcdat1/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgm2\_6/ptcdat1/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgm2\_6/ptcdat1/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgm2\_6/ptcdat1/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2830	99.7	541	US-10-757-832-3	Sequence 3, Appl1
2	982.5	34.6	542	US-10-950-163-30	Sequence 30, Appl1
3	958.5	33.8	530	US-10-314-739-3	Sequence 3, Appl1
4	958.5	33.8	530	US-10-895-791-2	Sequence 2, Appl1
5	958.5	33.8	530	US-10-895-791-6	Sequence 6, Appl1
6	958.5	33.8	530	US-10-895-791-7	Sequence 7, Appl1
7	953.5	33.6	530	US-10-950-163-28	Sequence 28, Appl1
8	953.5	33.6	530	US-10-950-163-29	Sequence 29, Appl1
9	260.5	9.2	669	US-10-209-507-2	Sequence 2, Appl1
10	252	8.9	668	US-10-209-507-4	Sequence 4, Appl1
11	249	8.8	547	US-10-670-695-4	Sequence 4, Appl1
12	249	8.8	671	US-10-670-695-2	Sequence 2, Appl1
13	249	8.8	671	US-10-769-531-1	Sequence 1, Appl1
14	248	8.7	668	US-10-769-531-2	Sequence 2, Appl1
15	247.5	8.7	667	US-10-769-531-3	Sequence 3, Appl1
16	142.5	5.0	618	US-10-769-531-4	Sequence 4, Appl1
17	118.5	4.2	736	US-10-863-637-7	Sequence 7, Appl1
18	117	4.1	3970	US-10-156-761-10429	Sequence 10429, A
19	116.5	4.1	1147	US-10-327-481A-38	Sequence 38, Appl1
20	115.5	4.1	511	US-10-080-170-641	Sequence 641, App
21	115.5	4.1	511	US-10-080-170-641	Sequence 641, App
22	115.5	4.1	511	US-10-468-356-641	Sequence 641, App
23	115.5	4.1	511	US-10-510-021-67	Sequence 67, Appl1
24	111	3.9	1203	US-10-369-493-8333	Sequence 8333, Ap
25	109.5	3.8	1693	US-09-851-410-7	Sequence 7, Appl1
26	108	3.8	5245	US-10-329-079-45	Sequence 45, Appl1
27	107	3.8	1073	US-10-925-357-7	Sequence 7, Appl1

28	104.5	3.7	2914	US-10-093-463-82	Sequence 82, Appl1
29	103	3.6	1700	US-09-734-402-2	Sequence 2, Appl1
30	102	3.6	1121	US-09-734-402-1	Sequence 1, Appl1
31	101.5	3.6	1073	US-10-156-761-8117	Sequence 8117, Ap
32	101	3.6	995	US-10-450-763-52543	Sequence 52543, A
33	100.5	3.5	1198	US-10-156-761-8467	Sequence 8467, Ap
34	100	3.5	307	US-09-815-242-5155	Sequence 5155, Ap
35	100	3.5	307	US-10-282-122A-43599	Sequence 43599, A
36	100	3.5	701	US-10-156-761-9875	Sequence 9875, Ap
37	99.5	3.5	894	US-09-223-490-34	Sequence 34, Appl1
38	99.5	3.5	894	US-09-236-939-34	Sequence 34, Appl1
39	99.5	3.5	894	US-10-646-760-34	Sequence 34, Appl1
40	99.5	3.5	894	US-10-696-909A-4	Sequence 4, Appl1
41	99.5	3.5	894	US-10-631-467-609	Sequence 609, App
42	99.5	3.5	1062	US-10-389-566-608	Sequence 608, App
43	99.5	3.5	1668	US-10-732-923-8865	Sequence 8865, Ap
44	99.5	3.5	1828	US-10-221-625-15	Sequence 15, Appl1
45	99.5	3.5	2971	US-10-146-473-50	Sequence 50, Appl1

## ALIGNMENTS

```

RESULT 1
US-10-757-832-3
Sequence 3, Application US/10757832
Publication No. US20050037016A1
GENERAL INFORMATION:
APPLICANT: VIRGIN, HERBERT W.
TITLE OF INVENTION: MURINE CALICIVIRUS
FILE REFERENCE: 56029-45752
CURRENT APPLICATION NUMBER: US/10/757, 832
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 60/440, 016
PRIOR FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 541
TYPE: PRT
ORGANISM: Murine Norovirus type 1
FEATURE:
NAME/KEY: misc feature
LOCATION: (32)..(32)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (52)..(52)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (106)..(106)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (291)..(291)
OTHER INFORMATION: Variable amino acid
US-10-757-832-3
Query Match 99.7%, Score 2830, DB 5, Length 541,
Best Local Similarity 100.0%, Pred. No. 2.1e-256,
Matches 541, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
Cy 1 MRMSDGAAPRANGSEASGCDLVPAAVEQAVPXPVAGALAAADAGQINQIXPWFQNFV 60
Db 1 MRMSDGAAPRANGSEASGCDLVPAAVEQAVPXPVAGALAAADAGQINQIXPWFQNFV 60
Cy 61 QCPVGRSISPRTPGSHLFDLALGRLNPLYLAHLSMTTGVGNKXEVQVLGNATFAG 120
Db 61 QCPVGRSISPRTPGSHLFDLALGRLNPLYLAHLSMTTGVGNKXEVQVLGNATFAG 120
Cy 121 KVVVALVPPPPPGSLTTAQITCPHYMCDVRLTLPQLFLVRRRLVHATDQESMR 180
Db 121 KVVVALVPPPPPGSLTTAQITCPHYMCDVRLTLPQLFLVRRRLVHATDQESMR 180

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using SW model

Run on: December 16, 2005, 14:12:48 / Search time 20.0539 Seconds  
(without alignments)  
2230.364 Million cell updates/sec

Title: US-10-757-832-3

Sequence: 1 MEMSDGAAPKANGSEASGQD.....PLUYOLASVGLATGMLKQ 541

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database:

Issued Patents AA:  
1: /cgn2\_6/prodata/1/1aa/5 COMB.pep.\*  
2: /cgn2\_6/prodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/8 COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/ECTUS\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/PR\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/Backfillseq1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	958.5	33.8	530	2	US-08-486-049-3
2	958.5	33.8	530	2	US-10-314-739A-3
3	260.5	9.2	669	2	US-09-617-594A-2
4	260.5	9.2	669	2	US-10-209-507-2
5	253	8.9	626	2	US-09-590-020-7
6	252	8.9	668	2	US-09-590-020-7
7	252	8.9	668	2	US-10-209-507-4
8	244	8.6	623	2	US-09-590-020-2
9	244	8.6	623	2	US-09-590-020-4
10	233	8.2	622	2	US-09-590-020-6
11	117.5	4.1	2318	2	US-09-091-219-24
12	117.5	4.1	2318	2	US-09-660-541-24
13	109.5	3.9	1042	2	US-09-252-991A-30444
14	109.5	3.9	1693	2	US-08-478-507-7
15	109.5	3.9	1693	2	US-09-128-275A-7
16	109.5	3.9	1693	2	US-09-553-427-7
17	108.5	3.8	3567	1	US-07-642-734C-4
18	108.5	3.8	3567	1	US-08-439-009A-4
19	103.5	3.6	2206	1	US-07-852-260-2
20	103.5	3.6	2206	1	US-08-461-503-2
21	103.5	3.6	2206	1	US-08-465-250-2
22	102	3.6	3457	1	US-08-416-603-4
23	100	3.5	755	2	US-09-252-991A-28386
24	99.5	3.5	894	1	US-08-372-892-2
25	99.5	3.5	894	1	US-08-445-640-34
26	99.5	3.5	894	2	US-08-170-558-34
27	99.5	3.5	894	2	US-08-447-314-34

28	99.5	3.5	894	2	US-08-445-461-34	Sequence 34, Appl
29	99.5	3.5	894	2	US-09-223-490-34	Sequence 34, Appl
30	99.5	3.5	975	2	US-09-949-016-7595	Sequence 7595, Ap
31	99.5	3.5	2872	2	US-09-579-181-2	Sequence 2, Appl
32	99.5	3.5	3118	2	US-09-579-181-1	Sequence 1, Appl
33	97.5	3.4	888	1	US-08-445-640-35	Sequence 35, Appl
34	97.5	3.4	888	2	US-08-170-558-35	Sequence 35, Appl
35	97.5	3.4	888	2	US-08-447-314-35	Sequence 35, Appl
36	97.5	3.4	888	2	US-08-445-461-35	Sequence 35, Appl
37	97.5	3.4	888	2	US-09-223-490-35	Sequence 35, Appl
38	96	3.4	723	2	US-09-893-737-100	Sequence 100, App
39	95.5	3.4	623	1	US-08-653-740-7	Sequence 7, Appl
40	95.5	3.4	623	1	US-09-073-594-7	Sequence 7, Appl
41	95.5	3.4	623	1	US-09-275-925-7	Sequence 7, Appl
42	95.5	3.4	3729	2	US-08-804-227C-4	Sequence 4, Appl
43	95	3.3	669	2	US-09-949-016-6887	Sequence 6887, Ap
44	95	3.3	677	2	US-09-949-016-8351	Sequence 8351, Ap
45	94.5	3.3	1206	2	US-09-252-991A-19632	Sequence 19632, A

## ALIGNMENTS

RESULT 1  
US-08-486-049-3  
Sequence 3, Application US/08486049  
Patent No. 6572862  
GENERAL INFORMATION:  
APPLICANT: Bates, Mary K  
APPLICANT: Jiang, Xi  
APPLICANT: Graham, David Y  
TITLE OF INVENTION: Method and Reagents to Detect and  
NUMBER OF SEQUENCES: 4  
TITLE OF INVENTION: Characterize No. 6572862walk and Related Viruses  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Fulbright & Jaworski L.L.P.  
STREET: 801 Pennsylvania Ave., N.W.  
CITY: Washington, D.C.  
STATE:  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,049  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Davis, Peter  
REGISTRATION NUMBER: 36, 119  
REFERENCE/DOCKET NUMBER: 311.023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-662-0200  
TELEFAX: 202-662-4643  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 530 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-049-3  
Query Match 33.8%, Score 958.5, DB 2, Length 530;  
Best Local Similarity 40.6%, Pred. No. 2.6e-91;  
Matches 223, Conservative 79, Mismatches 208, Indels 39, Gaps 11;  
QY 1 MEMSDGAAPKANGSEASGQDVFPA-VEQAVXPQVAGALAPAPAGQINQIXPMIFQNF 59  
DB 2 MWASDGAAPKANGSEASGQDVFPA-LVPEVNASDPLAMDVFVAGSSTAVATACGVNPIIDPTINNF 60

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:39:38 / Search time 79.532 Seconds  
(without alignments)  
2988.763 Million cell updates/sec

Title: US-10-757-832-3

Perfect score: 2838  
Sequence: 1 MEMSDGAPKANGSEASGQD.....PRLYLAVSGSLATGRLMKQ 541

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

A\_Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2830	99.7	541	9	ADY21360 Murine no
2	993.5	35.0	542	9	ADZ22153 Snow moun
3	990	34.9	535	4	AAB49707
4	980.5	34.5	539	4	AAB49704
5	980.5	34.5	544	4	AAB49703
6	968.5	34.1	542	4	AAB49708
7	967.5	34.1	546	4	AAB49702
8	963.5	33.9	540	4	AAB49706
9	962.5	33.9	530	4	AAB49701
10	962.5	33.9	530	9	ADZ22152
11	958.5	33.8	530	9	ADZ22151
12	958.5	33.8	530	7	ADZ22151
13	958.5	33.8	530	7	ADZ22151
14	958.5	33.8	530	9	ADZ22151
15	958.5	33.8	530	9	ADZ22151
16	958.5	33.8	530	9	ADZ22151
17	958.5	33.8	530	9	ADZ22151
18	951	33.5	545	4	AAB49700
19	934.5	33.0	548	4	AAB49705
20	934.5	32.9	548	2	AAB49709
21	933.5	32.9	548	5	AAB49709
22	923.5	32.5	550	4	AAB49709
23	837	29.5	541	4	AAB49710
24	303.5	10.7	579	2	AAB08143

25	260.5	9.2	669	4	AAB67461	AAB67461 Amino aci
26	252	8.9	668	4	AAB67462	AAB67462 Amino aci
27	249	8.8	547	4	AAM50108	AAM50108 Feline ca
28	249	8.8	671	4	AAM50107	AAM50107 Feline ca
29	249	8.8	671	8	AD574102	AD574102 Feline ca
30	248	8.7	668	8	AD574103	AD574103 Virulent
31	247.5	8.7	667	8	AD574104	AD574104 Virulent
32	247.5	8.7	668	8	AD574105	AD574105 Virulent
33	244	8.6	623	4	AAB47044	AAB47044 Feline ca
34	244	8.6	623	4	AAB47043	AAB47043 Feline ca
35	241	8.5	668	2	AAB10686	AAB10686 Feline ca
36	241	8.5	668	4	AAB04304	AAB04304 Feline ca
37	233	8.2	622	4	AAB47045	AAB47045 Feline ca
38	138	4.9	40	5	AAB91273	AAB91273 Normal v
39	123	4.3	40	5	AAB91274	AAB91274 Normal v
40	118.5	4.2	736	6	ADY77374	ADY77374 Foot-and-
41	118.5	4.2	1698	9	AB014663	AB014663 Novel hum
42	116.5	4.1	1147	5	AB876724	AB876724 Foot and
43	115.5	4.1	511	4	AAB19847	AAB19847 Mycobacte
44	115.5	4.1	511	5	ABU05990	ABU05990 M. tuberc
45	115.5	4.1	934	1	AAP20016	AAP20016 Sequence

## ALIGNMENTS

RESULT 1	ADY21360	standard; protein; 541 AA.
ID	ADY21360	
XX	ADY21360	
AC	ADY21360	
XX	ADY21360	
DT	05-MAY-2005	(first entry)
XX	05-MAY-2005	
DB	Murine norovirus 1 (NMV-1)	consensus DNA ORF2 protein.
XX	Murine norovirus 1	
XX	Diagnosis; enteritis; antiinflammatory; gastrointestinal-gen.;	
KW	Gastroenteritis; gastrointestinal disease; inflammation; virulence;	
KM	Vaccine; animal disease model.	
XX		
OS	Murine norovirus 1.	
XX		
PH	Key	Location/Qualifiers
FT	Misc-difference 32	/note= "Xaa equals variable amino acid"
FT	Misc-difference 52	/note= "Xaa equals variable amino acid"
FT	Misc-difference 106	/note= "Xaa equals variable amino acid"
FT	Misc-difference 291	/note= "Xaa equals variable amino acid"
FT	Misc-difference 291	/note= "Xaa equals variable amino acid"
XX	US2005037016-A1.	
XX	17-FEB-2005.	
XX	14-JAN-2004; 2004US-00757832.	
XX	14-JAN-2003; 2003US-0440016P.	
XX	(VIRG/) VIRGIN H W.	
XX	(VIRG/) VIRGIN H W.	
XX	Virgin HW;	
XX	WPI, 2005-161903/17.	
XX	N-PSDB; ADY21358.	
XX	New isolated polynucleotide encoding murine norovirus-1 (NMV-1) useful	
XX	for treating and/or preventing non-bacterial epidemic gastroenteritis	
XX	caused by murine noroviruses.	
XX	claim 13; SEQ ID NO 3; 42dp; English.	

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

M protein - protein search, using sw model

on on: December 16, 2005, 14:18:50 / Search time 1.57709 Seconds  
(without alignments)  
888.505 Million cell updates/sec

file: US-10-757-832-4

effect score: 1066  
sequence: 1 MAGALFAGIGGLMIGINS.....GGTYNGRFVSLPRIGSSRA 208

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 51470 seqs, 6736768 residues

total number of hits satisfying chosen parameters: 51470

intimum DB seq length: 0  
aximum DB seq length: 200000000

ost-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

atabase : Published Applications\_AA\_New\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.5	8.3	371	7	US-11-137-671-16
2	86.5	8.1	1263	7	US-11-076-163-3
3	83.5	7.8	1170	7	US-11-080-026-2
4	82.5	7.7	1255	7	US-11-022-562-235
5	81.5	7.6	758	6	US-10-485-517-144
6	80	7.5	406	6	US-10-821-234-1026
7	79	7.4	432	6	US-10-878-556A-72
8	78.5	7.4	394	6	US-10-467-657-4698
9	77.5	7.3	669	6	US-10-878-556A-87
10	77.5	7.3	757	7	US-11-110-082-35
11	76.5	7.2	781	7	US-11-194-246-344
12	76.5	7.2	1970	6	US-10-821-234-1641
13	75.5	7.1	451	6	US-10-995-561-886
14	74.5	7.0	463	6	US-10-793-626-960
15	74.5	7.0	1463	6	US-10-971-982-3
16	74	6.9	612	6	US-10-467-657-3988
17	74	6.9	859	7	US-11-188-743-16
18	73.5	6.9	358	6	US-10-995-561-885
19	73.5	6.9	358	6	US-10-995-561-885
20	73.5	6.9	388	6	US-10-995-561-889
21	73.5	6.9	388	6	US-10-995-561-887
22	73.5	6.9	405	7	US-11-083-551A-29
23	73.5	6.9	405	7	US-11-083-551A-50
24	73.5	6.9	473	6	US-10-793-626-548
25	73.5	6.9	1304	6	US-10-821-234-1648

26	72.5	6.8	761	7	US-11-110-082-34	Sequence 34, Appl
27	72	6.8	654	7	US-11-110-082-24	Sequence 24, Appl
28	72	6.8	3655	7	US-11-075-185-5	Sequence 5, Appl
29	71.5	6.7	509	6	US-10-821-234-1093	Sequence 1093, Ap
30	71	6.7	405	6	US-10-821-234-1357	Sequence 1357, Ap
31	70.5	6.6	416	6	US-10-793-626-2	Sequence 2, Appl
32	70.5	6.6	5024	6	US-10-793-626-2964	Sequence 2964, Ap
33	70	6.6	2504	6	US-10-647-956A-8	Sequence 8, Appl
34	69.5	6.5	268	6	US-10-510-386-180	Sequence 180, App
35	69.5	6.5	972	6	US-10-821-234-1587	Sequence 1587, Ap
36	69.5	6.5	1404	6	US-10-878-556A-169	Sequence 169, App
37	69	6.5	438	6	US-10-995-561-589	Sequence 589, App
38	69	6.5	477	6	US-10-995-561-587	Sequence 587, App
39	69	6.5	477	6	US-10-995-561-588	Sequence 588, App
40	69	6.5	2516	6	US-10-647-956A-2	Sequence 2, Appl
41	68.5	6.4	249	7	US-11-054-515-2049	Sequence 2049, Ap
42	68.5	6.4	894	6	US-10-485-517-416	Sequence 416, App
43	68.5	6.4	1290	6	US-10-485-517-141	Sequence 141, App
44	68	6.4	251	7	US-11-054-515-1812	Sequence 1812, Ap
45	68	6.4	481	7	US-11-116-939-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1  
US-11-137-671-16  
Sequence 16, Application US/11137671  
Publication No. US20050268350A1  
GENERAL INFORMATION:  
APPLICANT: Kirschbaum, Bernd  
Berglund, Erick  
Weisenernab, Michael  
Polites, Greg  
TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION COMPLEXES FROM TRANSGENIC NON-HUMAN ANIMALS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: HELLER, BIRMAN, WHITE & MCANULTY  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/137, 671  
FILING DATE: 25-May-2005  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/849, 243  
FILING DATE: 07-May-2001  
ATTORNEY/AGENT INFORMATION:  
NAME: Granados, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 38005-0148  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)912-2020  
TELEFAX: (202)912-2020  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-11-137-671-16  
Query Match 8.3%; Score 88.5; DB 7; Length 371.

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 16, 2005, 14:13:00 ; Search time 25.234 Seconds  
(without alignments)  
3444.190 Million cell updates/sec

Title: US-10-757-832-4

Perfect score: 1066  
Sequence: 1 MAGALFGAIGGIMGIIGNS.....OGTYTNGRVSLPKIGSSRA 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA Main:\*  
1: /cgn2\_6/prodata/1/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata/1/pubppaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/prodata/1/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/prodata/1/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1066	100.0	208	US-10-757-832-4	Sequence 4, Appl1
2	188	17.6	212	US-10-314-739-4	Sequence 4, Appl1
3	106.5	10.0	825	US-10-369-493-22501	Sequence 22501, A
4	104	9.8	2703	US-11-097-143-7590	Sequence 7590, A
5	103	9.7	494	US-09-833-790-234	Sequence 234, App
6	100	9.4	475	US-10-450-763-40845	Sequence 40845, A
7	97.5	9.1	1032	US-09-733-643-16	Sequence 16, Appl1
8	97.5	9.1	1032	US-10-120-801-64	Sequence 64, Appl1
9	97	9.1	551	US-10-437-963-152729	Sequence 152729, A
10	97	9.1	3828	US-10-732-823-15040	Sequence 15040, A
11	96.5	9.1	1146	US-10-437-963-110893	Sequence 110893, A
12	96.5	9.1	4823	US-10-051-874-169	Sequence 169, App
13	96	9.0	511	US-10-451-467A-468	Sequence 468, App
14	95.5	9.0	305	US-10-372-054-18	Sequence 18, Appl1
15	95.5	9.0	1013	US-11-097-143-39909	Sequence 39909, A
16	94.5	8.9	547	US-11-097-143-13383	Sequence 13383, A
17	93.5	8.8	748	US-10-437-963-125846	Sequence 125846, A
18	93.5	8.8	828	US-11-097-143-24114	Sequence 24114, A
19	93	8.7	413	US-10-424-599-240403	Sequence 240403, A
20	92	8.6	575	US-11-097-143-17316	Sequence 17316, A
21	92	8.6	584	US-10-382-122A-47689	Sequence 47689, A
22	92	8.6	1237	US-10-335-977-51163	Sequence 5116, App
23	91	8.5	183	US-10-424-599-194937	Sequence 194937, A
24	91	8.5	1112	US-10-450-763-52772	Sequence 52772, A
25	90	8.4	207	US-10-424-599-204198	Sequence 204198, A
26	90	8.4	347	US-10-282-122A-49941	Sequence 49941, A
27	89.5	8.4	355	US-10-425-115-342321	Sequence 342321, A

28	89.5	8.4	576	US-10-425-114-42381	Sequence 42381, A
29	89	8.3	560	US-10-425-115-306352	Sequence 306352, A
30	89	8.3	603	US-10-425-114-42780	Sequence 42780, A
31	89	8.3	975	US-11-097-143-8637	Sequence 8637, App
32	89	8.3	1448	US-10-408-765A-998	Sequence 998, App
33	88.5	8.3	338	US-09-933-638A-12	Sequence 12, Appl1
34	88.5	8.3	339	US-10-116-275-184	Sequence 184, App
35	88.5	8.3	339	US-10-818-694-2	Sequence 2, Appl1
36	88.5	8.3	345	US-10-818-694-15	Sequence 15, Appl1
37	88.5	8.3	371	US-09-849-243-16	Sequence 8257, App
38	88.5	8.3	468	US-10-739-930-8257	Sequence 8257, App
39	88.5	8.3	481	US-10-233-584A-3	Sequence 3, Appl1
40	88.5	8.3	641	US-10-233-584A-1	Sequence 1, Appl1
41	88.5	8.3	643	US-09-801-368-236	Sequence 236, App
42	88	8.3	318	US-10-351-891-126	Sequence 126, App
43	88	8.3	318	US-10-699-113-31	Sequence 31, Appl1
44	88	8.3	339	US-10-282-122A-45100	Sequence 45100, A
45	88	8.3	577	US-10-425-115-329192	Sequence 329192, A

#### ALIGNMENTS

```

RESULT 1
US-10-757-832-4
; Sequence 4, Application US/10757832
; Publication No. US20050037016A1
; GENERAL INFORMATION:
; APPLICANT: VIRGIN, HERBERT W.
; TITLE OF INVENTION: MURINE CALICIVIRUS
; FILE REFERENCE: 56029-45752
; CURRENT APPLICATION NUMBER: US/10/757,832
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 60/440,016
; PRIOR FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Murine Norovirus type 1
US-10-757-832-4

Query Match      100.0%; Score 1066; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.1e-94;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MAGALFGAIGGIMGIIGNSIVNOLANKOLAAQFGNSSLATOTIOAQDLTLMGQ 60
DB      1 MAGALFGAIGGIMGIIGNSIVNOLANKOLAAQFGNSSLATOTIOAQDLTLMGQ 60

QY      61 OFNOQLQTNPFKHELEMLGAOVQAOQAQENAINITPAOLQAAGFKTATRLALGCOPT 120
DB      61 OFNOQLQTNPFKHELEMLGAOVQAOQAQENAINITPAOLQAAGFKTATRLALGCOPT 120

QY      121 RAVDSGRTTYTANQVPTFGSGFTTTPGQVTSRPVDTSLPLISGRLPBLRGGSWS 180
DB      121 RAVDSGRTTYTANQVPTFGSGFTTTPGQVTSRPVDTSLPLISGRLPBLRGGSWS 180

QY      181 PRDHPATOGTYTNGRVSLPKIGSSRA 208
DB      181 PRDHPATOGTYTNGRVSLPKIGSSRA 208

RESULT 2
US-10-314-739-4
; Sequence 4, Application US/10314739
; Publication No. US20030129588A1
; GENERAL INFORMATION:
; APPLICANT: Estes, Mary K
; Jjiang, Xi
; Graham, David Y
; TITLE OF INVENTION: Methods and Reagents to Detect and

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 14:12:48 ; Search time 7.71019 Seconds  
(without alignments)  
2230.364 Million cell updates/sec

Title: US-10-757-832-4

Perfect score: 1066  
Sequence: 1 MAGALFGAIGGGLMIGINS.....GGTYNGRPVSLPRIGSSRA 208

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/6.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/H.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/RS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	17.6	212	US-08-486-049-4	Sequence 4, Appl
2	188	17.6	212	US-10-314-739A-4	Sequence 4, Appl
3	159.5	15.9	170	US-10-314-739A-6	Sequence 6, Appl
4	104	9.8	2703	US-08-185-432-19	Sequence 19, Appl
5	104	9.8	2703	US-08-899-232-4	Sequence 4, Appl
6	104	9.8	2703	US-09-121-457-4	Sequence 4, Appl
7	97.5	9.1	1032	US-09-733-643B-16	Sequence 16, Appl
8	95.5	9.0	305	US-09-339-159B-18	Sequence 18, Appl
9	89.5	8.4	624	US-08-947-965-78	Sequence 27, Appl
10	89.5	8.4	655	US-08-469-202-27	Sequence 27, Appl
11	89.5	8.4	655	US-08-469-202-28	Sequence 28, Appl
12	89.5	8.4	655	US-08-484-434C-34	Sequence 34, Appl
13	89.5	8.4	655	US-08-484-434C-35	Sequence 35, Appl
14	89.5	8.4	655	US-09-384-361-34	Sequence 34, Appl
15	89.5	8.4	655	US-09-384-361-35	Sequence 35, Appl
16	89	8.3	1108	US-09-538-092-29	Sequence 29, Appl
17	88.5	8.3	339	US-09-324-258-2	Sequence 2, Appl
18	88.5	8.3	339	US-09-538-092-964	Sequence 964, App
19	88.5	8.3	343	US-09-324-258-15	Sequence 15, Appl
20	88.5	8.3	643	US-09-196-270-3	Sequence 3, Appl
21	88.5	8.3	643	US-09-487-558B-236	Sequence 236, App
22	88	8.3	354	US-09-328-352-7262	Sequence 7262, Ap
23	86.5	8.1	732	US-09-270-767-44652	Sequence 44652, A
24	86.5	8.1	1463	US-09-949-016-11696	Sequence 11696, A
25	86.5	8.1	1464	US-08-891-640-2	Sequence 2, Appl
26	86.5	8.1	1464	US-09-949-016-6738	Sequence 6738, Ap
27	86.5	8.1	1464	US-09-842-256-2	Sequence 2, Appl

28	84.5	7.9	390	US-09-252-991A-17829	Sequence 17829, A
29	84.5	7.9	793	US-09-568-256-10	Sequence 10, Appl
30	84	7.9	314	US-09-328-352-4934	Sequence 4934, Ap
31	83.5	7.8	150	US-09-647-140B-23	Sequence 23, Appl
32	83.5	7.8	194	US-09-270-767-60105	Sequence 60105, A
33	83.5	7.8	589	US-10-261-164-2	Sequence 2, Appl
34	83.5	7.8	966	US-09-487-558B-372	Sequence 372, App
35	83.5	7.8	1065	US-08-630-172-9	Sequence 9, Appl
36	83.5	7.8	1065	US-09-375-419-9	Sequence 9, Appl
37	83.5	7.8	1170	US-08-789-078-2	Sequence 2, Appl
38	83.5	7.8	1170	US-08-752-633-2	Sequence 2, Appl
39	83.5	7.8	1170	US-10-261-164-1	Sequence 1, Appl
40	83.5	7.8	1170	PCT-US95-04886-2	Sequence 2, Appl
41	83	7.8	263	US-09-248-796A-23610	Sequence 23610, A
42	83	7.8	385	US-09-328-352-4372	Sequence 4372, Ap
43	83	7.8	675	US-09-248-796A-20699	Sequence 20699, A
44	83	7.8	801	US-09-351-150A-25	Sequence 25, Appl
45	83	7.8	865	US-09-902-540-10416	Sequence 10416, A

#### ALIGNMENTS

RESULT 1  
US-08-486-049-4  
; Sequence 4, Application US/08486049  
; Patent No. 6572862  
GENERAL INFORMATION:  
APPLICANT: Bates, Mary K  
APPLICANT: Jiang, Xi  
APPLICANT: Graham, David Y  
TITLE OF INVENTION: Methods and Reagents to Detect and  
TITLE OF INVENTION: Characterize No. 6572862walk and Related Viruses  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSES: Fulbright & Jaworski L.L.P.  
STREET: 801 Pennsylvania Ave., N.W.  
CITY: Washington, D.C.  
STATE:  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,049  
FILING DATE: June 7, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Davis, Peter  
REGISTRATION NUMBER: 36,119  
REFERENCE/DOCKET NUMBER: 311,023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-662-0200  
TELEFAX: 202-662-4643  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 212 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-049-4  
Query Match 17.6%; Score 188; DB-2; Length 212;  
Best local similarity 31.7%; Pred. No. 4.1e-12;  
Matches 60; Conservative 15; Mismatches 70; Indels 44; Gaps 6;  
1 MAGALFGAIGGGLMIGINSIVONTQANKQLAAGQFGNSLLATQIAQKDTLMQGO 60  
SALGAGCIQVGGKALASQ 33



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: December 16, 2005, 13:39:53 ; Search time 35.0463 Seconds  
(without alignments)  
4187.310 Million cell updates/sec

Title: US-10-757-832-4  
Perfect score: 1066  
Sequence: 1 MAGALFAGIGGIMGIGNS.....OGTYNGRFPVSLPIKIGSSRA 208

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1066	100.0	208	Q80J93_9CALI	Q80J93 murine novo
2	255.5	24.0	219	Q91164_9CALI	Q91164 human calic
3	254	23.8	258	Q917W7_9CALI	Q917W7 norwalk-11k
4	251	22.5	258	Q917X0_9CALI	Q917X0 norwalk-11k
5	248.5	23.3	257	Q918A9_9CALI	Q918A9 norwalk-11k
6	248.5	23.3	258	Q5F4T4_9CALI	Q5F4T4 norwalk-vir
7	247	23.2	259	Q80RDS_9CALI	Q80RDS snow mounta
8	246.5	23.1	257	Q91H08_9CALI	Q91H08 human calic
9	242.5	22.7	259	Q80X17_9CALI	Q80X17 norwalk-11k
10	242.5	22.7	259	Q8V780_9CALI	Q8V780 norwalk-vir
11	241.5	22.7	259	Q66294_9CALI	Q66294 human calic
12	240.5	22.6	258	Q6KD13_9CALI	Q6KD13 human calic
13	239.5	22.5	262	Q917W4_9CALI	Q917W4 norwalk-11k
14	238.5	22.4	242	Q917V5_9CALI	Q917V5 norwalk-11k
15	238	22.3	259	Q783X9_9CALI	Q783X9 norwalk-11k
16	238	22.3	259	Q8V783_9CALI	Q8V783 norwalk-vir
17	237.5	22.3	259	Q918B2_9CALI	Q918B2 norwalk-11k
18	236.5	22.2	268	Q91322_9CALI	Q91322 human calic
19	235.5	22.1	259	Q54AD5_9CALI	Q54AD5 human calic
20	235.5	22.1	268	Q6REW0_9CALI	Q6REW0 norwalk-11k
21	235.5	22.1	268	Q917W1_9CALI	Q917W1 norwalk-11k
22	233.5	21.9	242	Q917V8_9CALI	Q917V8 norwalk-11k
23	233.5	21.9	259	Q783X5_9CALI	Q783X5 norwalk-11k
24	233.5	21.9	259	Q8V777_9CALI	Q8V777 norwalk-vir
25	233.5	21.8	268	Q5XKY0_9CALI	Q5XKY0 norwalk-11k
26	232	21.8	216	Q7TBK9_9CALI	Q7TBK9 bovine ente
27	232	21.8	282	Q7BBL0_9CALI	Q7BBL0 bovine ente
28	231.5	21.7	258	Q918A6_9CALI	Q918A6 norwalk-11k
29	231.5	21.7	268	Q68538_9CALI	Q68538 norwalk-11k
30	231.5	21.7	268	Q6PP17_9CALI	Q6PP17 norwalk-11k
31	231.5	21.7	268	Q77080_9CALI	Q77080 canberwell

32	231.5	21.7	282	Q8B4Y8_9CALI	Q8B4Y8 norwalk-11k
33	230.5	21.6	268	Q6PPJ0_9CALI	Q6PPJ0 norwalk-11k
34	230.5	21.6	268	Q6PPJ3_9CALI	Q6PPJ3 norwalk-11k
35	230.5	21.6	268	Q6PPJ6_9CALI	Q6PPJ6 norwalk-11k
36	230.5	21.6	268	Q6PPJ9_9CALI	Q6PPJ9 norwalk-11k
37	230.5	21.6	268	Q6PPK2_9CALI	Q6PPK2 norwalk-11k
38	230.5	21.6	268	Q6PPK5_9CALI	Q6PPK5 norwalk-11k
39	230.5	21.6	268	Q6PPK8_9CALI	Q6PPK8 norwalk-11k
40	230.5	21.6	268	Q6PPJ1_9CALI	Q6PPJ1 norwalk-11k
41	230.5	21.6	268	Q6PPJ4_9CALI	Q6PPJ4 norwalk-11k
42	230.5	21.6	268	Q6PPJ7_9CALI	Q6PPJ7 norwalk-11k
43	230.5	21.6	268	Q6PPM0_9CALI	Q6PPM0 norwalk-11k
44	230.5	21.6	268	Q6PPM3_9CALI	Q6PPM3 norwalk-11k
45	230.5	21.6	268	Q6PPM6_9CALI	Q6PPM6 norwalk-11k

## ALIGNMENTS

RESULT 1	Q80J93_9CALI	PRELIMINARY;	PRT;	208 AA.
ID	Q80J93_9CALI	PRELIMINARY;	PRT;	208 AA.
AC	Q80J93_9CALI	PRELIMINARY;	PRT;	208 AA.
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Small basic protein.			
OS	Murine norovirus 1.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;			
OX	Norovirus.			
RN	NCBI_Taxid=223997;			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=22511930; PubMed=12624267; DOI=10.1126/science.1077905;			
RA	Karet S.M., Webus C.B., Lay M., Davidson J., Virgin H.W.;			
RT	"STAT1-dependent innate immunity to a Norwalk-like virus.";			
RL	Science 299:1575-1578 (2003).			
DR	EMBL; AY228235; AAO63100.1; -; Genomic_RNA.			
DR	InterPro; IPR004278; RNA_capsid.			
DR	Pfam; PF03035; RNA_capsid; 1.			
SQ	SEQUENCE 208 AA; 22073 MW; 9A33B823C665C01P CRC64;			
Query Match	100.0%; Score 1066; DB 2; Length 208;			
Best Local Similarity	100.0%; Pred. No. 2.8e-78;			
Matches	208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MAGALFAGIGGIMGIGNSISNVONTQNTKQLAAQFGYNSLATOIOAQKDLTMQ 60			
DB	1 MAGALFAGIGGIMGIGNSISNVONTQNTKQLAAQFGYNSLATOIOAQKDLTMQ 60			
QY	61 QPNQQLQNSFKHLEMLGAQVQAQAQENAINIKTAQLOAAGFSKTDATLALGQPT 120			
DB	61 QPNQQLQNSFKHLEMLGAQVQAQAQENAINIKTAQLOAAGFSKTDATLALGQPT 120			
QY	121 RAYDMSGRYYTANQPTVGFSGGFTPTTPGQVTSRPVDSPLPSGRLPSLGSWS 180			
DB	121 RAYDMSGRYYTANQPTVGFSGGFTPTTPGQVTSRPVDSPLPSGRLPSLGSWS 180			
QY	181 PRDHTPATQGTYNRFPVSLPIKIGSSRA 208			
DB	181 PRDHTPATQGTYNRFPVSLPIKIGSSRA 208			
RESULT 2	Q91164_9CALI	PRELIMINARY;	PRT;	219 AA.
ID	Q91164_9CALI	PRELIMINARY;	PRT;	219 AA.
AC	Q91164_9CALI	PRELIMINARY;	PRT;	219 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DR	Minor structural protein.			
OS	Human calicivirus NVV/MOH/99.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;			

